

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/003,608

DATE: 12/13/2001
TIME: 08:56:25

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\12132001\I003608.raw

4 <110> APPLICANT: Bartha, Gabor
5 Walker, Michael
W--> 7 *L1207 ↑ move up* Does Not Comply
W--> 8 METHODS FOR ANALYZING GENE EXPRESSION PATTERNS
Corrected Diskette Needed
12 <130> FILE REFERENCE: ICYTP012
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/003,608
C--> 14 <141> CURRENT FILING DATE: 2001-11-01
14 <150> PRIOR APPLICATION NUMBER: 60/245,081
15 <151> PRIOR FILING DATE: 2000-11-01
17 <160> NUMBER OF SEQ ID NOS: 30
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 4588
23 <212> TYPE: DNA
24 <213> ORGANISM: Human
26 <400> SEQUENCE: 1
27 gcggccgcca agagagatca caccccccagc cgaccctgcc agcgagcgag cccgacccca 60
28 ggctccatg gagcgtcgcc tccgccccgt ccctggcccg accccccgct gcggcgccgc 120
29 tcctgccttg accaggactt gggactttgc gaaagatcg cggggcccg agaggtaacc 180
30 gccgcgcctc cggagaggt gttggagagc acaatggctg aacaagtctt tcctcaggct 240
31 ttgtatttga gcaatatgcg gaaagctgtg aagatacggg agagaactcc agaagacatt 300
32 tttaaaccta ctaatggat cattcatcat tttaaaacca tgcaccgata cacactggaa 360
33 atgttcagaa cttgcagtt ttgcctca tttcgggaga tcatccacaa agccctcatc 420
34 gacagaaaaca tccaggccac cctggaaagc cagaagaaac tcaactggtg tcgagaagtc 480
35 cggaaagctt gggcgctgaa aacgaacggt gacggcaatt gcctcatgca tgccacttct 540
36 cagtacatgt gggcggttca ggacacagac ttggtaactga ggaaggcgt gttcagcacg 600
37 ctcaaggaaa cagacacacg caactttaaa ttccgctggc aactggatc tctcaaattct 660
38 caggaatttg ttgaaacggg gctttgtat gatactcgga actggaaatga tgaatggac 720
39 aatcttataca aaatggcttc cacagacaca cccatggccc gaagtggact tcagtacaac 780
40 tcactggaaag aaatacacat atttgcctt tgcaacatcc tcagaaggcc aatcattgtc 840
41 atttcagaca aaatgctaag aagttggaa tcaggttcca atttcgcctt tttgaaagtg 900
42 ggtggaaattt acttgcctt ccactggctt gcccaggaaat gctacagata cccattgtt 960
43 ctcggctatg acagccatca ttttgtaccc ttggtaaccc tgaaggacag tgggcctgaa 1020
44 atcccgagctt ttccacttgt taacagagac cggggaaatg ttgaagactt aaaagttcac 1080
45 ttttgcacat atcctgaaaaa tgagatgaag gagaagctct taaaagatgtt cttaatggtg 1140
46 atagaaatcc ccttccaaagg ctgggaccat ggcacaactc atctcatcaa tgccgcaaaag 1200
47 ttggatgaag ctaacttacc aaaagaaatc aatctggtag atgattactt tgaacttgc 1260
48 cagcatgagt acaagaaaatg gcaggaaaac agcgagcagg ggaggagaga ggggcacgccc 1320
49 cagaatccca tggAACCTTC cgtccccccag ctttctctca tggatgtaaa atgtgaaacg 1380
50 cccaaactgcc ctttccat gtctgtgaac acccagccctt tatgccatga gtgctcagag 1440
51 aggcggcaaa agaataaaaaa caaactccca aagctgaact ccaagccggg ccctgaggggg 1500
52 ctccctggca tggcgctcggttgccttcgg ggagaagcctt atgagccctt ggcgtggaaac 1560
53 cctgaggagt ccactggggg gcctcattcg gccccaccga cagcacccag ccctttctg 1620
54 ttcaatgttca gcaatgttccat gaaatgtcagg agccccggctt gccccttac actgaatgtg 1680
55 cagcacaacg gatgttgc acgttgcac aacgccccggc aacttcacgc cagccacgccc 1740
56 ccagaccaca caaggactt gatcccccggg aagtgcctca ggcctcctcc 1800
57 aggacatttca atggatctg cagttacttgc ttcaaaaagga ctacagcaga ggcctcctcc 1860

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105 <210> SEQ ID NO: 2

106 <211> LENGTH: 790

107 <212> TYPE: PRT

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108 <213> ORGANISM: Human
110 <400> SEQUENCE: 2
111 Met Ala Glu Gln Val Leu Pro Gln Ala Leu Tyr Leu Ser Asn Met Arg
112 1 5 10 15
113 Lys Ala Val Lys Ile Arg Glu Arg Thr Pro Glu Asp Ile Phe Lys Pro
114 20 25 30
115 Thr Asn Gly Ile Ile His His Phe Lys Thr Met His Arg Tyr Thr Leu
116 35 40 45
117 Glu Met Phe Arg Thr Cys Gln Phe Cys Pro Gln Phe Arg Glu Ile Ile
118 50 55 60
119 His Lys Ala Leu Ile Asp Arg Asn Ile Gln Ala Thr Leu Glu Ser Gln
120 65 70 75 80
121 Lys Lys Leu Asn Trp Cys Arg Glu Val Arg Lys Leu Val Ala Leu Lys
122 85 90 95
123 Thr Asn Gly Asp Gly Asn Cys Leu Met His Ala Thr Ser Gln Tyr Met
124 100 105 110
125 Trp Gly Val Gln Asp Thr Asp Leu Val Leu Arg Lys Ala Leu Phe Ser
126 115 120 125
127 Thr Leu Lys Glu Thr Asp Thr Arg Asn Phe Lys Phe Arg Trp Gln Leu
128 130 135 140
129 Glu Ser Leu Lys Ser Gln Glu Phe Val Glu Thr Gly Leu Cys Tyr Asp
130 145 150 155 160
131 Thr Arg Asn Trp Asn Asp Glu Trp Asp Asn Leu Ile Lys Met Ala Ser
132 165 170 175
133 Thr Asp Thr Pro Met Ala Arg Ser Gly Leu Gln Tyr Asn Ser Leu Glu
134 180 185 190
135 Glu Ile His Ile Phe Val Leu Cys Asn Ile Leu Arg Arg Pro Ile Ile
136 195 200 205
137 Val Ile Ser Asp Lys Met Leu Arg Ser Leu Glu Ser Gly Ser Asn Phe
138 210 215 220
139 Ala Pro Leu Lys Val Gly Ile Tyr Leu Pro Leu His Trp Pro Ala
140 225 230 235 240
141 Gln Glu Cys Tyr Arg Tyr Pro Ile Val Leu Gly Tyr Asp Ser His His
142 245 250 255
143 Phe Val Pro Leu Val Thr Leu Lys Asp Ser Gly Pro Glu Ile Arg Ala
144 260 265 270
145 Val Pro Leu Val Asn Arg Asp Arg Gly Arg Phe Glu Asp Leu Lys Val
146 275 280 285
147 His Phe Leu Thr Asp Pro Glu Asn Glu Met Lys Glu Lys Leu Leu Lys
148 290 295 300
149 Glu Tyr Leu Met Val Ile Glu Ile Pro Val Gln Gly Trp Asp His Gly
150 305 310 315 320
151 Thr Thr His Leu Ile Asn Ala Ala Lys Leu Asp Glu Ala Asn Leu Pro
152 325 330 335
153 Lys Glu Ile Asn Leu Val Asp Asp Tyr Phe Glu Leu Val Gln His Glu
154 340 345 350
155 Tyr Lys Lys Trp Gln Glu Asn Ser Glu Gln Gly Arg Arg Glu Gly His
156 355 360 365
157 Ala Gln Asn Pro Met Glu Pro Ser Val Pro Gln Leu Ser Leu Met Asp

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158	370	375	380
159	Val Lys Cys Glu Thr Pro Asn Cys Pro Phe Phe Met Ser Val Asn Thr		
160	385	390	395 400
161	Gln Pro Leu Cys His Glu Cys Ser Glu Arg Arg Gln Lys Asn Gln Asn		
162	405	410	415
163	Lys Leu Pro Lys Leu Asn Ser Lys Pro Gly Pro Glu Gly Leu Pro Gly		
164	420	425	430
165	Met Ala Leu Gly Ala Ser Arg Gly Glu Ala Tyr Glu Pro Leu Ala Trp		
166	435	440	445
167	Asn Pro Glu Glu Ser Thr Gly Gly Pro His Ser Ala Pro Pro Thr Ala		
168	450	455	460
169	Pro Ser Pro Phe Leu Phe Ser Glu Thr Thr Ala Met Lys Cys Arg Ser		
170	465	470	475 480
171	Pro Gly Cys Pro Phe Thr Leu Asn Val Gln His Asn Gly Phe Cys Glu		
172	485	490	495
173	Arg Cys His Asn Ala Arg Gln Leu His Ala Ser His Ala Pro Asp His		
174	500	505	510
175	Thr Arg His Leu Asp Pro Gly Lys Cys Gln Ala Cys Leu Gln Asp Val		
176	515	520	525
177	Thr Arg Thr Phe Asn Gly Ile Cys Ser Thr Cys Phe Lys Arg Thr Thr		
178	530	535	540
179	Ala Glu Ala Ser Ser Ser Leu Ser Thr Ser Leu Pro Pro Ser Cys His		
180	545	550	555 560
181	Gln Arg Ser Lys Ser Asp Pro Ser Arg Leu Val Arg Ser Pro Ser Pro		
182	565	570	575
183	His Ser Cys His Arg Ala Gly Asn Asp Ala Pro Ala Gly Cys Leu Ser		
184	580	585	590
185	Gln Ala Ala Arg Thr Pro Gly Asp Arg Thr Gly Thr Ser Lys Cys Arg		
186	595	600	605
187	Lys Ala Gly Cys Val Tyr Phe Gly Thr Pro Glu Asn Lys Gly Phe Cys		
188	610	615	620
189	Thr Leu Cys Phe Ile Glu Tyr Arg Glu Asn Lys His Phe Ala Ala Ala		
190	625	630	635 640
191	Ser Gly Lys Val Ser Pro Thr Ala Ser Arg Phe Gln Asn Thr Ile Pro		
192	645	650	655
193	Cys Leu Gly Arg Glu Cys Gly Thr Leu Gly Ser Thr Met Phe Glu Gly		
194	660	665	670
195	Tyr Cys Gln Lys Cys Phe Ile Glu Ala Gln Asn Gln Arg Phe His Glu		
196	675	680	685
197	Ala Lys Arg Thr Glu Glu Gln Leu Arg Ser Ser Gln Arg Arg Asp Val		
198	690	695	700
199	Pro Arg Thr Thr Gln Ser Thr Ser Arg Pro Lys Cys Ala Arg Ala Ser		
200	705	710	715 720
201	Cys Lys Asn Ile Leu Ala Cys Arg Ser Glu Glu Leu Cys Met Glu Cys		
202	725	730	735
203	Gln His Pro Asn Gln Arg Met Gly Pro Gly Ala His Arg Gly Glu Pro		
204	740	745	750
205	Ala Pro Glu Asp Pro Pro Lys Gln Arg Cys Arg Ala Pro Ala Cys Asp		
206	755	760	765

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207 His Phe Gly Asn Ala Lys Cys Asn Gly Tyr Cys Asn Glu Cys Phe Gln
208 770 775 780

209 Phe Lys Gln Met Tyr Gly
210 785 790

213 <210> SEQ ID NO: 3

214 <211> LENGTH: 1224

215 <212> TYPE: DNA

216 <213> ORGANISM: Human

218 <220> FEATURE:

219 <221> NAME/KEY: misc_feature
220 <222> LOCATION: 36, 91, 645, 655, 660, 671, 672

221 <223> OTHER INFORMATION: n = A,T,C or G

223 <221> NAME/KEY: misc_feature

224 <222> LOCATION: 36, 91, 645, 655, 660, 671, 672

225 <223> OTHER INFORMATION: n = A,T,C or G

227 <221> NAME/KEY: allele

228 <222> LOCATION: (0)...(0)

230 <400> SEQUENCE: 3

W--> 231 tcgggatcga tctggagctc cgggaatttc cctggncgg gactccgggc tttccagccc 60

W--> 232 caaccatgca taaaagggt tcggcggttcc nggagagcca cagagcccg gccacaggca 120

233 gctccgtgcc agctcttctt ctcctcteac agccggcaga cccgcgtct gagccccat 180

234 ggccccgcgt gctctctccg ccgcggcccg caatccccgg ctctgcgag tggcgctgt 240

235 gctctgtcgtc ctggtagccg ctggccggcg cgcagcagga ggcggccctgg ccactgaact 300

236 gcgctgcca gtcgtgcaga ccctgcaggg aattcacctc aagaacatcc aaagtgtgaa 360

237 ggtgaagtcc cccgacccc actgcgcaca aaccgaagtc atagccacac tcaagaatgg 420

238 gcagaaaagct tgtctcaacc ccgcacatcgcc catgtttaag aaaatcatcg aaaagatgt 480

239 gaaaaatggc aaatccaact gaccagaagg aaggaggaag cttattgtg gctgttcctg 540

240 aaggaggccc tgcccttaca ggaacagaag agaaaagaga gacacagctg cagaggccac 600

W--> 241 ctgggattgc gcctaattgtg tttgagcatc acttaggaga aggcncggat taatnatttn 660

W--> 242 attaatttat nnattgggtt gttttagaag attctatgtt aatattttat gtgtaaaata 720

243 aggttatgtat tgaatctact tgcacactct cccattatat ttattgtta ttttaggtca 780

244 aacccaagg tggtaatcc tgattcatat ttaatttggaa gatagaaggt ttgcagat 840

245 tctctagtca tttgttaata tttcttctgt atgacatatac acatgtcagc cactgtgata 900

246 gaggctgagg aatccaagaa aatggccagt aagatcaatg tgacggcagg gaaatgtatg 960

247 tggatgttatt ttgttaactgt aaagatgaat gtcagttgtt atttattgaa atgatttcac 1020

248 agtgtgttgtt caacatttct catgttgaag cttaagaac taaaatgttc taaatatccc 1080

249 ttggacattt tatgtcttcc ttgttaaggca tactgccttg tttaatgtta attatgcagt 1140

250 gtttccctt gtgttagagc agagaggttt cgatattttat tgatgtttc acaaagaaca 1200

1224

251 gaaaaataaaa atattnaaaa atat

253 <210> SEQ ID NO: 4

254 <211> LENGTH: 107

255 <212> TYPE: PRT

256 <213> ORGANISM: Human

258 <400> SEQUENCE: 4

259 Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu

260 1 5 10 15

261 Arg Val Ala Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala

262 20 25 30

263 Ala Gly Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr

delete - duplicate

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/003,608

DATE: 12/13/2001
TIME: 08:56:26

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\12132001\I003608.raw

L:7 M:201 W: Mandatory field data missing, TITLE INVENTION
L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:486 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11